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## RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/988,745

TIME: 18:58:12

Input Set : N:\Crf3\RULE60\09988745.raw

Output Set: N:\CRF3\01152002\I988745.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: LI, Yi and RUBEN, Steven

7 (ii) TITLE OF INVENTION: HUMAN AMINE RECEPTOR

9 (iii) NUMBER OF SEQUENCES: 10

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.

13 (B) STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

14 (C) CITY: WASHINGTON

15 (D) STATE: DC

16 (E) COUNTRY: UNITED STATES OF AMERICA

17 (F) ZIP: 20005-3934

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk

21 (B) COMPUTER: IBM PC compatible

22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

25 (vi) CURRENT APPLICATION DATA:

C--&gt; 26 (A) APPLICATION NUMBER: US/09/988,745

C--&gt; 27 (B) FILING DATE: 20-Nov-2001

28 (C) CLASSIFICATION:

C--&gt; 30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: 09/314,006

32 (B) FILING DATE:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: STEFFE, ERIC K

36 (B) REGISTRATION NUMBER: 36,688

37 (C) REFERENCE/DOCKET NUMBER: 1488.0840001

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (202) 371-2600

41 (B) TELEFAX: (202) 371-2540

## 44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 1380 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: double

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

55 (ix) FEATURE:

56 (A) NAME/KEY: CDS

57 (B) LOCATION: 252..1262

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 CTAGAGCTAG CAGGAGTAAC TCTCATGGAA CCTTGGAAAC CATTCTTCAA TTGAATTTCA 60

64 GGGCACATTT GAATCAGTAC CCAGGGGCAC TGTACTATGC TCCCAGCTGG ACCTTAGTTT 120

66 CCTCCTCCTC GTTTCACCCCT GTGAGTAATT AACAGACAAA ATTTTTTTTTT TTTTTTTTTT 180

68 TTTTTTTTTT TTTTGGCCCT CCAGTGGAGA AGGTGGCCAG TTCTCAGACA GAGGAAGAGT 240

70 AGAAATCATA A ATG AGA GCT GTC TTC ATC CAA GGT GCT GAA GAG CAC CCT 290

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71          Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro
72          1          5          10
74 GCG GCA TTC TGC TAC CAG GTG AAT GGG TCT TGC CCC AGG ACA GTA CAT      338
75 Ala Ala Phe Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His
76      15          20          25
78 ACT CTG GGC ATC CAG TTG GTC ATC TAC CTG ACC TGT GCA GCA GGC ATG      386
79 Thr Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met
80      30          35          40          45
82 CTG ATT ATC GTG CTA GGG AAT GTA TTT GTG GCA TTT GCT GTG TCC TAC      434
83 Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr
84          50          55          60
86 TTC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC TCC CTG GCC      482
87 Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala
88          65          70          75
90 CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTG CCC CTC AGC ACC ATT      530
91 Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile
92          80          85          90
94 CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG      578
95 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu
96          95          100          105
98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC      626
99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu
100 110          115          120          125
102 TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC      674
103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu
104          130          135          140
106 TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA      722
107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala
108          145          150          155
110 GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT      770
111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp
112          160          165          170
114 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG      818
115 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val
116          175          180          185
118 GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC      866
119 Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe
120 190          195          200          205
122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG      914
123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
124          210          215          220
126 ATC TTT GTG GTT GCT ACC AGA CAG GCT CAG CAG ATT ACC ACA TTG AGC      962
127 Ile Phe Val Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser
128          225          230          235
130 AAA AGC CTG GCT GGG GCT GCC AAG CAT GAG AGA AAA GCT GCC AAG ACC      1010
131 Lys Ser Leu Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr
132          240          245          250
134 CTG GGC ATT GTT GTG GGC ATA TAC CTC TTG TGC TGG CTG CCC TTC ACC      1058
135 Leu Gly Ile Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr

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136      255      260      265
138 ATA GAC ACG ATG GTC GAC AGC CTC CTT CAC TTT ATC ACA CCC CCA CTG      1106
139 Ile Asp Thr Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu
140 270      275      280      285
142 GTC TTT GAC ATC TTT ATC TGG TTT GCT TAC TTC AAC TCA GCC TGC AAC      1154
143 Val Phe Asp Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn
144      290      295      300
146 CCC ATC ATC TAT GTC TTT TCC TAC CAG TGG TTT CGG AAG GCA CTG AAA      1202
147 Pro Ile Ile Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys
148      305      310      315
150 CTC ACA CTG AGC CAG AAG GTC TTC TCA CCG CAG ACA CGC ACT GTT GAT      1250
151 Leu Thr Leu Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp
152      320      325      330
154 TTG TAC CAA GAA TGATTCCTTC TACTAAATGC AGGCAAGGAG TAGGACCTCA      1302
155 Leu Tyr Gln Glu
156      335
158 CAGGAAAGAT AAGTGGCACT GTGACCGCGG GCTGTGTGGT GTTGAGTTTG TGGGCATGCT      1362
160 TCCAGGACAG CATGGGTT      1380
163 (2) INFORMATION FOR SEQ ID NO: 2:
165     (i) SEQUENCE CHARACTERISTICS:
166         (A) LENGTH: 337 amino acids
167         (B) TYPE: amino acid
168         (D) TOPOLOGY: linear
170     (ii) MOLECULE TYPE: protein
172     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
174 Met Arg Ala Val Ile Gln Gly Ala Glu His Pro Ala Ala Phe
175 1      5      10      15
177 Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His Thr Leu Gly
178      20      25      30
180 Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met Leu Ile Ile
181      35      40      45
183 Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr Phe Lys Ala
184      50      55      60
186 Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala Leu Ala Asp
187 65      70      75      80
189 Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile Arg Ser Val
190      85      90      95
192 Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu His Thr Tyr
193      100      105      110
195 Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu Cys Phe Ile
196      115      120      125
198 Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu Tyr Pro Ser
199      130      135      140
201 Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala Gly Trp Gly
202 145      150      155      160
204 Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp Val Val Glu
205      165      170      175
207 Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val Gly Ser Cys
208      180      185      190

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210 Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe Pro Leu Phe  
 211           195                           200                           205  
 213 Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys Ile Phe Val  
 214           210                           215                           220  
 216 Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser Lys Ser Leu  
 217 225                           230                           235                           240  
 219 Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile  
 220                           245                           250                           255  
 222 Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr Ile Asp Thr  
 223                           260                           265                           270  
 225 Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu Val Phe Asp  
 226           275                           280                           285  
 228 Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn Pro Ile Ile  
 229           290                           295                           300  
 231 Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys Leu Thr Leu  
 232 305                           310                           315                           320  
 234 Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp Leu Tyr Gln  
 235                           325                           330                           335  
 237 Glu

240 (2) INFORMATION FOR SEQ ID NO: 3:

242 (i) SEQUENCE CHARACTERISTICS:

243 (A) LENGTH: 29 base pairs

244 (B) TYPE: nucleic acid

245 (C) STRANDEDNESS: single

246 (D) TOPOLOGY: linear

248 (ii) MOLECULE TYPE: DNA (genomic)

253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

255 CGGAATTCCT UATGAGAGCT GTCTTCATC

29

257 (2) INFORMATION FOR SEQ ID NO: 4:

259 (i) SEQUENCE CHARACTERISTICS:

260 (A) LENGTH: 32 base pairs

261 (B) TYPE: nucleic acid

262 (C) STRANDEDNESS: single

263 (D) TOPOLOGY: linear

265 (ii) MOLECULE TYPE: DNA (genomic)

270 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

272 CGGAAGCTTC GTCATTCTTG GTACAAATCA AC

32

274 (2) INFORMATION FOR SEQ ID NO: 5:

276 (i) SEQUENCE CHARACTERISTICS:

277 (A) LENGTH: 30 base pairs

278 (B) TYPE: nucleic acid

279 (C) STRANDEDNESS: single

280 (D) TOPOLOGY: linear

282 (ii) MOLECULE TYPE: DNA (genomic)

287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

289 CGGGATCCCT CCATGAGAGC TGTCTTCATC

30

291 (2) INFORMATION FOR SEQ ID NO: 6:

293 (i) SEQUENCE CHARACTERISTICS:

294 (A) LENGTH: 29 base pairs

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295      (B) TYPE: nucleic acid
296      (C) STRANDEDNESS: single
297      (D) TOPOLOGY: linear
299      (ii) MOLECULE TYPE: DNA (genomic)
304      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
306 CGGGATCCCG CTCATTCTTG GTACAAATC      29
308 (2) INFORMATION FOR SEQ ID NO: 7:
310      (i) SEQUENCE CHARACTERISTICS:
311          (A) LENGTH: 34 base pairs
312          (B) TYPE: nucleic acid
313          (C) STRANDEDNESS: single
314          (D) TOPOLOGY: linear
316      (ii) MOLECULE TYPE: DNA (genomic)
321      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
323 GTCCAAGCTT GCCACCATGA GAGCTGTCTT CATC      34
325 (2) INFORMATION FOR SEQ ID NO: 8:
327      (i) SEQUENCE CHARACTERISTICS:
328          (A) LENGTH: 61 base pairs
329          (B) TYPE: nucleic acid
330          (C) STRANDEDNESS: single
331          (D) TOPOLOGY: linear
333      (ii) MOLECULE TYPE: DNA (genomic)
338      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
340 CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCATTCTTGG TACAAATCAA      60
342 C      61
344 (2) INFORMATION FOR SEQ ID NO: 9:
346      (i) SEQUENCE CHARACTERISTICS:
347          (A) LENGTH: 365 amino acids
348          (B) TYPE: amino acid
349          (C) STRANDEDNESS: Not Relevant
W--> 350      (D) TOPOLOGY: Not Relevant
352      (ii) MOLECULE TYPE: protein
357      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
359 Ala Arg Leu Leu Val Leu Ala Ser Pro Pro Ala Ser Leu Leu Pro Pro
360 1      5      10      15
362 Ala Ser Glu Gly Ser Ala Pro Leu Ser Gln Gln Trp Thr Ala Gly Met
363      20      25      30
365 Gly Leu Leu Val Ala Leu Ile Val Leu Leu Ile Val Val Gly Asn Val
366      35      40      45
368 Leu Val Ile Val Ala Ile Ala Lys Thr Pro Arg Leu Gln Thr Leu Thr
369      50      55      60
371 Asn Leu Phe Ile Met Ser Leu Ala Ser Ala Asp Leu Val Met Gly Leu
372      65      70      75      80
374 Leu Val Val Pro Phe Gly Ala Thr Ile Val Val Trp Gly Arg Trp Glu
375      85      90      95
377 Tyr Gly Ser Phe Phe Cys Glu Leu Trp Thr Ser Val Asp Val Leu Cys
378      100      105      110
380 Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala Leu Asp Arg Tyr
381      115      120      125

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## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09988745.raw

Output Set: N:\CRF3\01152002\I988745.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:350 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9